

Clone name	SEQ ID NO	Enantioselectivity for Neryl Butyrate (N) or Geranyl Butyrate (G)
1f15 (G2)	21	G
3C12	22	G
3N19 (G2)	23	G
G2.2	24	G
2C3	25	G
2F11	26	G
KV11 (6C7)	27	N
KV6 (3A1)	28	N
KV2 (2D1)	29	N
N2.5	30	N
KV5 (2H6)	31	N
3E5	32	G
G2.1	33	G
3H24 (G2)	34	G
KV10 (4G6)	35	N
KV12 (6D4)	36	N
N2.2	37	N
N2.3	38	N
N2.1	39	N
KV4 (2E12)	40	N
KV9 (4C6)	41	N
7D6	42	G
3F3	43	G
2D11 (G2)	44	G
3C23 (G2)	45	G
G2.3	46	G
2A3	47	G
2F4	48	G
2B9 (G2)	49	G
2C5	50	G
KV1 (2A6)	51	N
2D13 (G2)	52	G
3C8	53	G
2D5	54	G

FIGURE 1

Clone Name	E value for Neryl Butyrate	E value for Geranyl Butyrate
Exemplar (sgc2 and sgd2)	---	2.1
Exemplar (2h6)	1.4	---
Exemplar (14g14)	1.8	---
Exemplar (3f19a11)	2.2	(not tested)
Exemplar (3e5)	---	3.0
Exemplar (3n19)	---	3.8

FIGURE 2

FIGURE 2

SEQ: 001-405 (pumilus)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC
SEQ: 002-406 (subtilis)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC
SEQ: 003-402 (megat.)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC
SEQ: 004-400 (lentus)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC
SEQ: 005-396 (circul.)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC
SEQ: 006-392 (azotof.)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC
SEQ: 007-398 (firmus)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC
SEQ: 008-393 (badius)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC
SEQ: 009-Dc5h	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC
SEQ: 010-Dc5f	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC
SEQ: 011-Dc5c1	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC
SEQ: 012-Dc5a2	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC
SEQ: 013-Dc512	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC
SEQ: 014-Sga	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC
SEQ: 015-Sgc	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC
SEQ: 016-Sgd	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC
SEQ: 017-Sgf	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC
SEQ: 018-Sgh	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC
SEQ: 019-Mt2b1	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC
SEQ: 020-H2a	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC

Figure 3a

Figure 1 consists of 12 micrographs arranged in a 4x3 grid, showing the development of a single embryo from fertilization to hatching. The first row shows the fertilized egg and early cleavage stages. The second row shows the embryo with a visible yolk and developing structures. The third row shows the embryo with a more defined head and tail. The fourth row shows the hatched embryo with a fully formed head and tail.

	(Signal peptide coding region)	(Mature coding region)	
SEQ: 001-405 (pumilus)	76	150	
SEQ: 002-406 (subtilis)	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 003-402 (megat.)	(65)	TGTTTGCATTGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 004-400 (lentus)	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GA - CACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 005-396 (ciroleul.)	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 006-392 (azotof.)	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 007-398 (firmus)	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 008-393 (badius)	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 009-Dc5h	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 010-Dc5f	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 011-Dc5c1	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 012-Dc5a2	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 013-Dc512	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 014-Sga	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 015-Sgc	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 016-Sgd	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 017-Sgf	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 018-Sgh	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 019-Mt2b1	(75)	CTTCATCCAGCCAAAGAAATCAA - GCAGCT	GAGCACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT
SEQ: 020-H2a	(65)	TGTTTGCATGCAGCCGTCAGCAAAAAGCCGCT	GAACACAATCCAGTCTTTATGGTTTCAC - GGTAATCGAGGAGCT

Figure 3b

SEQ: 001-405 (pumilus) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 002-406 (subtilis) (139) TCATTCAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 003-402 (megat.) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 004-400 (lentus) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 005-396 (circul.) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 006-392 (azotof.) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 007-398 (firmus) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 008-393 (badius) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 009-Dc5h (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 010-Dc5f (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 011-Dc5c1 (148) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 012-Dc5a2 (148) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 013-Dc512 (148) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 014-Sga (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 015-Sgc (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 016-Sgd (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 017-Sgf (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 018-Sgh (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 019-Mt2b1 (148) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT
 SEQ: 020-H2a (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

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Figure 3c

SEQ:001-405 (pumilus) (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:002-406 (subtilis) (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGACCGGTATTACACGATTTGTGCAAAAAGGTTTGTAGATGAA
 SEQ:003-402 (megat..) (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:004-400 (lentus) (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:005-396 (circul..) (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:006-392 (azotof..) (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:007-398 (firmus) (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:008-393 (badius) (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:009-Dc5h (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:010-Dc5f (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:011-Dc5c1 (223) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:012-Dc5a2 (223) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:013-Dc512 (223) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:014-Sga (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:015-Sgc (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:016-Sgd (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:017-Sgf (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:018-Sgh (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:019-Mt2b1 (223) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA
 SEQ:020-H2a (214) TTTTGGGACAAAGACAGGACGAAATTATAACAAATGGCCCGGTATTATACGATTTGTGCAAAAAGGTTTGTAGACGAA

Figure 3d

301
 SEQ:001-405 (pumilus) (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGTATGGGTGGCGCGAACACACACCTTACTACATAAAAAATCTG
 SEQ:002-406 (subtilis) (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:003-402 (megat.) (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:004-400 (lentus) (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:005-396 (circul.) (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:006-392 (azotof.) (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:007-398 (firmus) (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:008-393 (badius) (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:009-Dc5h (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:010-Dc5f (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:011-Dc5c1 (298) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:012-Dc5a2 (298) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:013-Dc512 (298) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:014-Sga (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:015-Sgc (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:016-Sgd (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:017-Sgf (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:018-Sgh (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:019-Mt2b1 (298) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG
 SEQ:020-H2a (289) ACGGGTGCAGAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACACTTTACTACATAAAAAATCTG

Figure 3e

SEQ: 001-405 (pumilus) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGGTTTCGACGACAAAGCAAGGCGCTTCCG
 SEQ: 002-406 (subtilis) (364) GACGGCGGAAATAAAGTTGAAAACGTCGTGACGCTTGGCGGCGGAAACCGTTTGACGACAGGCAAGGCGCTTCCG
 SEQ: 003-402 (megat.) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 004-400 (lentus) (364) GACGGCGGAAATAAAATTGAAAACGCTGTAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 005-396 (circul.) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 006-392 (azotof.) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 007-398 (firmus) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 008-393 (badius) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 009-Dc5h (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 010-Dc5f (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 011-Dc5c1 (373) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 012-Dc5a2 (373) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 013-Dc512 (373) GATGGCGGCGATAAAAATTGAGAACGTTGTCAAAATTGGTGAGCAAAACGGACTCGTTATCACTCAGAGCATATACCA
 SEQ: 014-Sga (364) GATGGCGGTAATAAAATTGAAAACGTTGTTCACAAATTGGTGAGCAAAACGGACTCGTTTGACAGGCAAGGCGCTTCCG
 SEQ: 015-Sgc (364) GATGGCGGTAATAAAATTGAAAACGTCGTAAACACTTGGCGGCGGAAATCGTCTTGTACAGGCAAGGCGCTTCCG
 SEQ: 016-Sgd (364) GATGGCGGTAATAAAATTGAAAACGTCGTAAACACTTGGCGGCGGAAATCGTCTTGTACAGGCAAGGCGCTTCCG
 SEQ: 017-Sgf (364) GATGTTGGCGATAAAAAATTGAGAACGTTGTCACAATTGGTGAGCAAAACGGACTCGTTTCAAGCAGAGCATATACCA
 SEQ: 018-Sgh (364) GATGTTGGCGATAAAAAATTGAGAACGTTGTCACAATTGGTGAGCAAAACGGACTCGTTTCAAGCAGAGCATATACCA
 SEQ: 019-Mt2b1 (373) GATGCGGCGATAAAAAATTGAAAACGTCGTCAACCATTTGGTGAGCAAAACGGACTCGTTTCAAGCAGAGCATATACCA
 SEQ: 020-H2a (364) GATGCGGCGATAAAAAATTGAGAACGTTGTCACAAAATTGGCGGAGCAAAACGGACTCGTTTCAAGCAGAGCATATACCA

Figure 3f

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SEQ: 001-405 (pumilus) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTTACATGATGTCATGAATTTACTTT
 SEQ: 002-406 (subtilis) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 003-402 (negat.) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 004-400 (lentus) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 005-396 (circul.) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 006-392 (azotof.) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 007-398 (firmus) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 008-393 (badius) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 009-Dc5h (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 010-Dc5f (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 011-Dc5c1 (448) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 012-Dc5a2 (448) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 013-Dc512 (448) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 014-Sga (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 015-Sgc (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 016-Sgd (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 017-Sgf (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 018-Sgh (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 019-Mt2b1 (448) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT
 SEQ: 020-H2a (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATCCATTTACATGATGTCATGAATTTACTTT

Figure 39

SEQ:001-405 (pumilus)	(586)	601	GTCAACAGCCTGATTAAAGAAAGGACTGAACGGCGGGGGCCAAAATACGAATTAA
SEQ:002-406 (subtilis)	(586)		GTCAACAGCCTGATTAAAGAAAGGCTGAACGGCGGGGACTCAATACAAAATTAG
SEQ:003-402 (megat.)	(586)		GTCAACAGCCTGATTAAAGAAAGGACTGAACGGCGGGGGCCACAAATACAAATTAA
SEQ:004-400 (lentus)	(586)		GTCAACAGCCTGATTAAAGAAAGGACTGAACGGCGGGAGGACTAAATACAAATTAA
SEQ:005-396 (circul.)	(586)		GTCAACAGCCTGATTAAAGAAAGGACTGAACGGCGGGGGCTCAATACAAATTAA
SEQ:006-392 (azotof.)	(586)		GTCAACAGCCTGATTAAAGAAAGGACTGAACGGCGGGGGCTAGATACAAATTAA
SEQ:007-398 (firmus)	(586)		GTCAACAGCCTGATTAAAGAAAGGACTGAACGGCGGGAGGCCACAAATACAAATTAA
SEQ:008-393 (badius)	(586)		GTCAACAGCCTGATTAAAGAAAGGCTGAACGGCGGGGGCTCAATACAAATTAA
SEQ:009-Dc5h	(586)		GTGAAAGGGTATTAAAGAAAGGACTGAACGGCGGGAGGGCTCAATACAAATTAA
SEQ:010-Dc5f	(586)		GTCAAAGGCTATGTGAAAGAAAGGATTGAATGGCGGGGGACAGAATACAAATTAA
SEQ:011-Dc5c1	(595)		GTCAAAGGCTATATCAAAGAAAGGACTGAATGGCGGGGGAGGCCAAAATACAAATTAA
SEQ:012-Dc5a2	(595)		GTGAAAGGGTATTAAAGAAAGGACTGAACGGCGGGAGGGCTCAATACAAATTAA
SEQ:013-Dc512	(595)		GTCAACAGCCTGATTAAAGAAAGGCTTAACGGCGGGAGGGCTCAATACAAATTAA
SEQ:014-Sga	(586)		GTCAATAGCCTGATTAAAGAAAGGCTTAACGGCGGGAGGACTCAATACGAATTAA
SEQ:015-Sgc	(586)		GTCAACAGCCTGATTAAAGAAAGGCTTAACGGCGGGGGCTGAATACGAATTAA
SEQ:016-Sgd	(586)		GTCAAGGATATATTAAAGAAAGGACTGAACGGCGGGGGCTCAATACAAATTAA
SEQ:017-Sgf	(586)		GTCAAGGATATATTAAAGAAAGGACTGAACGGCGGGAGGGCCAAAATACAAATTAA
SEQ:018-Sgh	(586)		GTGAAAGGGTATTAAAGAAAGGACTGAACGGCGGGGGCTAAATACAAATTAA
SEQ:019-Mt2b1	(595)		GTCAAAGGATATATTAAAGAAAGGACTGAACGGCGGGGGACTAAATACAAATTAA
SEQ:020-H2a	(589)		

Figure 3i

SEQ: 021-1f15 (G2)	1	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAAATTTTTCGGGAAATTAAGAGCTATCT
SEQ: 022-3C12	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAAATTTTTCGGGAAATTAAGAGCTATCT
SEQ: 023-3N19 (G2)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAAATTTTTCGGGAAATTAAGAGCTATCT
SEQ: 024-G2.2	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAAATTTTTCGGGAAATTAAGAGCTATCT
SEQ: 025-2C3	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAAATTTTTCGGGAAATTAAGAGCTATCT
SEQ: 026-2F11	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 027-KV1.1 (6C7)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 028-KV6 (3A1)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 029-KV2 (2D1)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 030-N2.5	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 031-KV5 (2H6)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 032-3E5	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 033-G2.1	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 034-3H24 (G2)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 035-KV10 (4G6)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 036-KV12 (6D4)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 037-N2.2	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 038-N2.3	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 039-N2.1	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 040-KV4 (2E12)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 041-KV9 (4C6)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 042-7D6	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 043-3F3	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 044-2D11 (G2)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 045-3C23 (G2)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 046-G2.3	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 047-2A3	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 048-2F4	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 049-2B9 (G2)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 050-2C5	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 051-KV1 (2A6)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 052-2D13 (G2)	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 053-3C8	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT
SEQ: 054-2D5	(1)	TGAACACAAATCCAGTTGTTATGGTTACCGGTATTTGAGGGGCATCATTCAGTTTTCGGGAAATTAAGAGCTATCT

Figure 4a

SEQ: 021-1f15 (G2)	(76)	CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 022-3C12	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 023-3N19 (G2)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 024-G2.2	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 025-2C3	(76)	CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 026-2F11	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 027-KV11 (6C7)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 028-KV6 (3A1)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 029-KV2 (2D1)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 030-N2.5	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 031-KV5 (2H6)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 032-3E5	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 033-G2.1	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 034-3H24 (G2)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 035-KV10 (4G6)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 036-KV12 (6D4)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 037-N2.2	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 038-N2.3	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 039-N2.1	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 040-KV4 (2E12)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 041-KV9 (4C6)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 042-7D6	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 043-3F3	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 044-2D11 (G2)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 045-3C23 (G2)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 046-G2.3	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 047-2A3	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 048-2F4	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 049-2B9 (G2)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 050-2C5	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 051-KV1 (2A6)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 052-2D13 (G2)	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 053-3C8	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 054-2D5	(76)	CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA

Figure 4b

SEQ: 021-1f15 (G2) (151) TGGCCCGGTATTATCGCGTTTTGTGAAAAAGGTATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 022-3C12 (151) TGGCCCGGTATTATCTAGATTCTGTCAAAGATGTGCTAGACAAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 023-3N19 (G2) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGATGAAACCGGTGCGAAAAAAGTGGACATTGTTCGCTCA
SEQ: 024-G2.2 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 025-2C3 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 026-2F1.1 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 027-KV1.1 (6C7) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 028-KV6 (3A1) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 029-KV2 (2D1) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 030-N2.5 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 031-KV5 (2H6) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 032-3E5 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 033-G2.1 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 034-3H24 (G2) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 035-KV1.0 (4G6) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 036-KV1.2 (6D4) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 037-N2.2 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 038-N2.3 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 039-N2.1 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 040-KV4 (2E12) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 041-KV9 (4C6) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 042-7D6 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 043-3F3 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 044-2D1.1 (G2) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 045-3C23 (G2) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 046-G2.3 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 047-2A3 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 048-2F4 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 049-2B9 (G2) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 050-2C5 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 051-KV1 (2A6) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 052-2D13 (G2) (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 053-3C8 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA
SEQ: 054-2D5 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTATTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTTCGCTCA

Figure 4c

226
SEQ: 021-1f15 (G2) (226) CAGCATGGGCGGCGTAAACACGCTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 022-3C12 (226) CAGCATGGGCGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 023-3N19 (G2) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 024-G2.2 (226) CAGCATGGGCGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 025-2C3 (226) CAGCATGGGCGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 026-2F11 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 027-KV11 (6C7) (226) CAGTATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 028-KV6 (3A1) (226) CAGTATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 029-KV2 (2D1) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 030-N2.5 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 031-KV5 (2H6) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 032-3E5 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 033-G2.1 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 034-3H24 (G2) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 035-KV10 (4G6) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 036-KV12 (6D4) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 037-N2.2 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 038-N2.3 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 039-N2.1 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 040-KV4 (2E12) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 041-KV9 (4C6) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 042-7D6 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 043-3F3 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 044-2D11 (G2) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 045-3C23 (G2) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 046-G2.3 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 047-2A3 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 048-2F4 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 049-2B9 (G2) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 050-2C5 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 051-KV1 (2A6) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 052-2D13 (G2) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 053-3C8 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 054-2D5 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC

Figure 4d

301
SEQ: 021-1f15 (G2) (301) GCTTGGCGGACGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 022-3C12 (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 023-3N19 (G2) (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 024-G2.2 (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 025-2C3 (301) CATTTGGTGGAGCAACCGGACTTCGTTTCAAGCAGAGCATACAGGCAAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 026-2F11 (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 027-KV11 (6C7) (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 028-KV6 (3A1) (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 029-KV2 (2D1) (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 030-N2.5 (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 031-KV5 (2H6) (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 032-3E5 (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 033-G2.1 (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 034-3H24 (G2) (301) ACTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 035-KV10 (4G6) (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 036-KV12 (6D4) (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 037-N2.2 (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 038-N2.3 (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 039-N2.1 (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 040-KV4 (2E12) (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 041-KV9 (4C6) (301) ACTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 042-7D6 (301) ACTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 043-3F3 (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 044-2D11 (G2) (301) ACTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 045-3C23 (G2) (301) ACTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 046-G2.3 (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 047-2A3 (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 048-2F4 (301) ACTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 049-2B9 (G2) (301) ACTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 050-2C5 (301) ACTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 051-KV1 (2A6) (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 052-2D13 (G2) (301) GCTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 053-3C8 (301) ACTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
SEQ: 054-2D5 (301) ACTTGGCGGCGGAAACCGTTTCGACGACAAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC

Figure 4e

SEQ: 021-1f15 (G2) (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 022-3C12 (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGGTAAAAATGTTCAAAAT
SEQ: 023-3N19 (G2) (376) ATCCATTTACGGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 024-G2.2 (376) ATCCATTTACGGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 025-2C3 (376) ATCCGTTTACAGCTAGCTAGCAGATCTTATTGTGCTCAACAGCTCTCTCTCGTTTAAATTTGGCGCAAGAAACGTTCCAAAT
SEQ: 026-2F11 (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 027-KV11 (6C7) (376) ATCCGTTTACAGTAGTGTGATATGATTGTGTTATGAATTTACTTTATCAAAATTTAGACGGGTAAAAATGTTCAAAAT
SEQ: 028-KV6 (3A1) (376) ATCCGTTTACAGTAGTGTGATATGATTGTGTTATGAATTTACTTTATCAAAATTTAGACGGGTAAAAATGTTCAAAAT
SEQ: 029-KV2 (2D1) (376) ATCCGTTTACAGTAGTGTGCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGGTAAAAATGTTCAAAAT
SEQ: 030-N2.5 (376) ATCCGTTTACAGTAGTGTGATATGATTGTGTTATGAATTTACTTTATCAAAATTTAGACGGGTAAAAATGTTCAAAAT
SEQ: 031-KV5 (2H6) (376) ATCCGTTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 032-3E5 (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGGTAAAAATGTTCAAAAT
SEQ: 033-G2.1 (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 034-3H24 (G2) (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 035-KV10 (4G6) (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 036-KV12 (6D4) (376) ATCCGTTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 037-N2.2 (376) ATCCGTTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 038-N2.3 (376) ATCCGTTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 039-N2.1 (376) ATCCGTTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 040-KV4 (2E12) (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 041-KV9 (4C6) (376) ATCCATTTACAGCAGTCCCGATATGTTGTCAATGAATTTACTTTATCAAAATTTAGACGGGTAAAAATGTTCAAAAT
SEQ: 042-7D6 (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 043-3F3 (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 044-2D11 (G2) (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 045-3C23 (G2) (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 046-G2.3 (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTGCTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 047-2A3 (376) ATCCGTTTACAGTAGTGTGATATGATTGTTATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 048-2F4 (376) ATCCGTTTACAGTAGTGTGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 049-2B9 (G2) (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGGTAAAAATGTTCAAAAT
SEQ: 050-2C5 (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 051-KV1 (2A6) (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 052-2D13 (G2) (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 053-3C8 (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT
SEQ: 054-2D5 (376) ATCCATTTACAGCAGTCCCGATATGATTGTCAATGAATTTACTTTATCAAAATTTAGACGGTGCCTAAAAATGTTCAAAAT

Figure 4 f

451

SEQ: 021-1f15 (G2) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 022-3C12 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 023-3N19 (G2) (451) CCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 024-G2.2 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 025-2C3 (451) CCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 026-2F11 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 027-KV11 (6C7) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 028-KV6 (3A1) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 029-KV2 (2D1) (451) TCATGGTTCGGACATATCGGCTTCTGTACAGCAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 030-N2.5 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 031-KV5 (2H6) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 032-3E5 (451) CCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 033-G2.1 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 034-3H24 (G2) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 035-KV10 (4G6) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 036-KV12 (6D4) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 037-N2.2 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 038-N2.3 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 039-N2.1 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 040-KV4 (2E12) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 041-KV9 (4C6) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 042-7D6 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 043-3F3 (451) CCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 044-2D11 (G2) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 045-3C23 (G2) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 046-G2.3 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 047-2A3 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 048-2F4 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 049-2B9 (G2) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 050-2C5 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 051-KV1 (2A6) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 052-2D13 (G2) (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 053-3C8 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG
 SEQ: 054-2D5 (451) TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAGGACTGAACGGCGG

Figure 4g

	526	544
SEQ: 021-1f15 (G2)	(526)	GGGACTCAATACGAATTGA
SEQ: 022-3C12	(526)	GGGACTCAATACGAATTGA
SEQ: 023-3N19 (G2)	(526)	GGGACTGAATACAAATTGA
SEQ: 024-G2.2	(526)	GGGACTCAATACGAATTGA
SEQ: 025-2C3	(526)	GGGCCACAATACGAATTGA
SEQ: 026-2F11	(526)	AGGCTAAATACGAATTGA
SEQ: 027-KV11 (6C7)	(526)	GGGCTTAAATACAAATTGA
SEQ: 028-KV6 (3A1)	(526)	GGGCTTAAATACAAATTGA
SEQ: 029-KV2 (2D1)	(526)	GGGCCAAAATACAAATTGA
SEQ: 030-N2.5	(526)	GGGCCACAATACAAATTGA
SEQ: 031-KV5 (2H6)	(526)	GGGCTGAATACAAATTGA
SEQ: 032-3E5	(526)	GGGCTCAATACGAATTGA
SEQ: 033-G2.1	(526)	GGGACTCAATACGAATTGA
SEQ: 034-3H24 (G2)	(526)	GGGACTCAATACGAATTGA
SEQ: 035-KV10 (4G6)	(526)	GGGCCACAATACAAATTGA
SEQ: 036-KV12 (6D4)	(526)	AGGCCACAATACAAATTGA
SEQ: 037-N2.2	(526)	AGGCCACAATACAAATTGA
SEQ: 038-N2.3	(526)	AGGCCACAATACAAATTGA
SEQ: 039-N2.1	(526)	AGGCCACAATACAAATTGA
SEQ: 040-KV4 (2E12)	(526)	GGGCCACAATACAAATTGA
SEQ: 041-KV9 (4C6)	(526)	GGGCCACAATACGAATTGA
SEQ: 042-7D6	(526)	GGGATTAAATACGAATTGA
SEQ: 043-3F3	(526)	GGGCCAGAATACGAATTGA
SEQ: 044-2D11 (G2)	(526)	AGGCCAGAATACGAATTGA
SEQ: 045-3C23 (G2)	(526)	GGGCCACAATACGAATTGA
SEQ: 046-G2.3	(526)	GGGCCAGAATACGAATTGA
SEQ: 047-2A3	(526)	AGGCTAAATACAAATTGA
SEQ: 048-2F4	(526)	AGGCCAGAATACGAATTGA
SEQ: 049-2B9 (G2)	(526)	AGGCCAAAATACGAATTGA
SEQ: 050-2C5	(526)	AGGCCAAAATACGAATTGA
SEQ: 051-KV1 (2A6)	(526)	GGGCCAGAATACGAATTGA
SEQ: 052-2D13 (G2)	(526)	AGGCCAAAATACGAATTGA
SEQ: 053-3C8	(526)	GGGCCAAAATACAAATTGA
SEQ: 054-2D5	(526)	AGGACAAAATACAAATTGA

Figure 4 h

	(Signal peptide)	(Mature region)	
	-35	-1	40
SEQ: 055-405 (pumilus)	(1) --MKFVKRRRIIALVTILVLSVTSLSLFAMQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 056-406 (subtilis)	(1) --MKFVKRRRIIALVTILVLSVTSLSLFALQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 057-402 (megat.)	(1) --MKFVKRRRIIALVTILVLSVTSLSLFAMQP-SAKAA	DTIQLLWFTGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 058-400 (lentus)	(1) --MKFVKRRRIIALVTILVLSVTSLSLFAMQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 059-396 (circul.)	(1) --MKFIKRRRIIALVTILVLSVTSLSLFAMQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 060-392 (azotof.)	(1) --MKFVKRRRIIALVTILVLSVTSLSLFAMQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 061-398 (firmus)	(1) --MKFVKRRRIIALVTILVLSVTSLSLFAMQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 062-393 (badius)	(1) --MKFVKRRRIIALVTILVLSVTSLSLFAMQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 063-Dc5h	(1) --MKFVKRRRIIALVTILVLSVTSLSLFALQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 064-Dc5f	(1) --MKFVKRRRIIALVTILVLSVTSLSLFALQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 065-Dc5c1	(1) MKVIFVKRRSLQIILVALALVLSIAFIQPKAKAA	EHNPPVVMVHGIGGASYNFASIKRYLVSQGWDQNQLFAIDF	
SEQ: 066-Dc5a2	(1) MKVIFVKRRSLQIILVALALVLSIAFIQPKAIRAA	EHNPPVVMVHGIGGASYNFASIKRYLVSQGWDQNQLFAIDF	
SEQ: 067-Dc512	(1) MKVIFVKRRSLQIILVALALVLSIAFIQPKAKAA	EHNPPVVMVHGIGGASYNFASIKRYLVSQGWDQNQLFAIDF	
SEQ: 068-Sga	(1) --MKFVKRRRIIALVTILVLSVTSLSLFALQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 069-Sgc	(1) --MKFVKRRRIIALVTILVLSVTSLSLFALQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 070-Sgd	(1) --MKFVKRRRIIALVTILVLSVTSLSLFALQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 071-Sgf	(1) --MKFVKRRRIIALVTILVLSVTSLSLFALQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 072-Sgh	(1) --MKFVKRRRIIALVTILVLSVTSLSLFALQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 073-Mt2b1	(1) MKVIFVKRRSLQIILVALALVLSIAFIQPKAIRAA	EHNPPVVMVHGIGGASYNFASIKRYLVSQGWDQNQLFAIDF	
SEQ: 074-H2a	(1) --MKFVKRRRIIALVTILVLSVTSLSLFALQP-SAKAA	EHNPPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	

Figure 5a

41

SEQ: 055-405 (pumilus)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	PYYI	KNLD	GGNKI	ENVV	TLGG	ANRST	TSKALPG
SEQ: 056-406 (subtilis)	(73)	WDKTGTNYNNGPVL	PRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKV	ANV	VT	TLGG	ANRLTTGKALPG
SEQ: 057-402 (megat.)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TLGG	ANRLTTGKALPG
SEQ: 058-400 (lentus)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TLGG	ANRLTTGKALPG
SEQ: 059-396 (circul.)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TLGG	ANRLTTGKALPG
SEQ: 060-392 (azotof.)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TLGG	ANRLTTGKALPG
SEQ: 061-398 (firmus)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TLGG	ANRLTTGKALPG
SEQ: 062-393 (badius)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TLGG	ANRLTTGKALPG
SEQ: 063-Dc5h	(73)	KDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TLGG	ANRLTTGKALPG
SEQ: 064-Dc5f	(73)	XDKTGNNRNGPRL	SRFVKDVL	DKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKV	ENV	VT	TLGG	ANRLTTGKALPG
SEQ: 065-Dc5c1	(76)	IDKTGNNLNGPRL	SRFVKDVL	LAKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	IGG	ANGLVSSRALPG
SEQ: 066-Dc5a2	(76)	IDKTGNNRNGPRL	SRFVKDVL	LAKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	IGG	ANGLVSLRALPG
SEQ: 067-Dc512	(76)	IDKTGNNRNGPRL	SRFVKDVL	DKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	IGG	ANGLVSSRALPG
SEQ: 068-Sga	(73)	RDKTGNNLNGPVL	SRFVKDVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TLGG	ANRLVTGKALPG
SEQ: 069-Sgc	(73)	WDKTGNNLNGPVL	SRFVKDVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TLGG	ANRLVTGKALPG
SEQ: 070-Sgd	(73)	SDKTGNNLNGPVL	SRFVKDVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TLGG	ANRLVTGKALPG
SEQ: 071-Sgf	(73)	KDKTGNNRNGPRL	SRFVKDVL	DKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	IGG	ANGLVSSRALPG
SEQ: 072-Sgh	(73)	IDKTGNNRNGPRL	SRFVKDVL	DKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	IGG	ANGLVSSRALPG
SEQ: 073-Mt2b1	(76)	IDKTGNNRNGPRL	SRFVKDVL	DKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	IGG	ANGLVSLRALPG
SEQ: 074-H2a	(73)	RDKTGNNRNGPRL	SKFVKDVL	DKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	IGG	ANGLVSSRALPG

Figure 5b

SEQ: 055-405 (pumilus)	(148)	116	TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNAQIHGVGHI GLLMNSQVNSLIKEGLNGGGQNTN	181
SEQ: 056-406 (subtilis)	(148)		TDPNQKILYTSIYSSADMIVN- YLSRLDGARNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGGLNTN	
SEQ: 057-402 (megat.)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN	
SEQ: 058-400 (lentus)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGGLNTN	
SEQ: 059-396 (circul.)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGGLNTN	
SEQ: 060-392 (azotof.)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGGLDTN	
SEQ: 061-398 (firmus)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNAQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN	
SEQ: 062-393 (badius)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN	
SEQ: 063-Dc5h	(148)		TDPNQKILYTSIYSSADMIVMN- YLSRLDGARNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGGLNTN	
SEQ: 064-Dc5f	(148)		TDPNQKILYTSVYSSADLIIVN- SLSRLIGARNILIHGVGHI GLTSSQVKGYIKEGLNGGGGLNTN	
SEQ: 065-Dc5c1	(151)		TDPNQKILYTSVYSSADLIIVN- SLSRLIGARNVLIHGVGHI GLTSSQVKGYIKEGLNGGGQNTN	
SEQ: 066-Dc5a2	(151)		TDPNQKILYTSVYSSADLIIVN- SLSRLIGARNVLIHGVGHI GLTSSQVKGYIKEGLNGGGQNTN	
SEQ: 067-Dc512	(151)		TDPNQKILYTSVYSSADLIIVN- SLSQFNWRKKHPDPGVGHI GLTSSQVKGYIKEGLNGGGGLNTN	
SEQ: 068-Sga	(148)		TDPNQKILYTSVYSSADMIVMN- YLTCLDGAKNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGGLNTN	
SEQ: 069-Sgc	(148)		TDPNQKILYTSVYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGGLNTN	
SEQ: 070-Sgd	(148)		TDPNQKILYTSVYSSADLIIVN- SLSRLIGARNVQIHGVGHI GLTSSQVKGYIKEGLNGGGGLNTN	
SEQ: 071-Sgf	(148)		TDPNQKILYTSVYSSADLIIVN- SLSRLIGARNVQIHGVGHI GLTSSQVKGYIKEGLNGGGGLNTN	
SEQ: 072-Sgh	(148)		TDPNQKILYTSVYSSADLIIVN- SLSRLIGARNVQIHGVGHI GLTSSQVKGYIKEGLNGGGQNTN	
SEQ: 073-Mt2b1	(151)		TDPNQKILYTSVYSSADLIIVN- SLSRLTGARNVLIHGVGHI GLTSSQVKGYIKEGLNGGGGLNTN	
SEQ: 074-H2a	(148)		TDPNQKILYTSVKLSRSHCRQQLSFNWLQETVQIHGVGHI GLTSSQVKGYIKEGLNGGGGLNTN	

Figure 5c

SEQ: 075-1f15 (G2)	(76)	SMGGANTL YYIKNLDGKNKVENVVTLGGTNRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 076-3C12	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 077-3N19 (G2)	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYGSADMIVMNYLSKLDGAKNVQI
SEQ: 078-G2.2	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYGSADMIVMNYLSKLDGAKNVQI
SEQ: 079-2C3	(76)	SMGGANTL YYIKNLDGKNKIENVVTTGGANGLVSSRALPGTDPNQKILYTSVYSSADLIVVNSLSRLIGARNVQI
SEQ: 080-2F11	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSRALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 081-KV11 (6C7)	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSVYSSADMIVMNYLSKLDGAKNVQI
SEQ: 082-KV6 (3A1)	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSVYSSADMIVMNYLSKLDGAKNVQI
SEQ: 083-KV2 (2D1)	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSVYSSADMIVMNYLSKLDGAKNVQI
SEQ: 084-N2.5	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSVYSSADMIVMNYLSKLDGAKNVQI
SEQ: 085-KV5 (2H6)	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRLVTGKALPGTDPNQKILYASVYSSADMIVMNYLSKLDGAKNVQI
SEQ: 086-3E5	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 087-G2.1	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGTNRLTTSRALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 088-3H24 (G2)	(76)	SMGGANTL YYIKNLDGKNKVENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 089-KV10 (4G6)	(76)	SMGGANTL YYIKNLDGKNKVENVVTLGGANRLVTGKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 090-KV12 (6D4)	(76)	SMGGANTL YYIKNLDGKNKVENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 091-N2.2	(76)	SMGGANTL YYIKNLDGKNKVENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 092-N2.3	(76)	SMGGANTL YYIKNLDGKNKVENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 093-N2.1	(76)	SMGGANTL YYIKNLDGKNKVENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 094-KV4 (2E12)	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 095-KV9 (4C6)	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 096-7D6	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 097-3F3	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 098-2D11 (G2)	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 099-3C23 (G2)	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 100-G2.3	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 101-2A3	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 102-2F4	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 103-2B9 (G2)	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 104-2C5	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 105-KV1 (2A6)	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 106-2D13 (G2)	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 107-3C8	(76)	SMGGANTL YYIKNLDGKNKVENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 108-2D5	(76)	SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI

Figure 6b

SEQ: 075-1f15 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN	151	180
SEQ: 076-3C12	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN		
SEQ: 077-3N19 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN		
SEQ: 078-G2.2	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN		
SEQ: 079-2C3	(151)	HGVGHIGLLTSSQVKGYIKEGLNGGGHNTN		
SEQ: 080-2F11	(151)	HGVGHIGLLMNSQVKGYIKEGLNGGGLNTN		
SEQ: 081-KV11 (6C7)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN		
SEQ: 082-KV6 (3A1)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN		
SEQ: 083-KV2 (2D1)	(151)	HGVGHIGLLYSSQVNSLIKEGLNGGQNTN		
SEQ: 084-N2.5	(151)	HGVGHTGLMNSQVNSLIKEGLNGGGHNTN		
SEQ: 085-KV5 (2H6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN		
SEQ: 086-3E5	(151)	HGVGHIGLLYSSQVNSLIKEGLNGGGLNTN		
SEQ: 087-G2.1	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN		
SEQ: 088-3H24 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN		
SEQ: 089-KV10 (4G6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN		
SEQ: 090-KV12 (6D4)	(151)	HGVGHIGLLMNSQVNRLLIKEGLNGGGHNTN		
SEQ: 091-N2.2	(151)	HGVGHIGLLMNSQVNRLLIKEGLNGGGHNTN		
SEQ: 092-N2.3	(151)	HGVGHIGLLMNSQVNRLLIKEGLNGGGHNTN		
SEQ: 093-N2.1	(151)	HGVGHIGLLMNSQVNRLLIKEGLNGGGHNTN		
SEQ: 094-KV4 (2E12)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN		
SEQ: 095-KV9 (4C6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN		
SEQ: 096-7D6	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN		
SEQ: 097-3F3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN		
SEQ: 098-2D11 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN		
SEQ: 099-3C23 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN		
SEQ: 100-G2.3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN		
SEQ: 101-2A3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN		
SEQ: 102-2F4	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN		
SEQ: 103-2B9 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN		
SEQ: 104-2C5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN		
SEQ: 105-KV1 (2A6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN		
SEQ: 106-2D13 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN		
SEQ: 107-3C8	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN		
SEQ: 108-2D5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN		

Figure 6c